SEQUENCE LISTING

<110> Chiorini, John
Kotin, Robert M.
Safer, Brian
Davidson, Elizabeth
Zabner, Joseph

<120> AAV5 VECTOR FOR TRANSDUCING BRAIN CELLS AND LUNG CELLS

<130> 14014.0323U2

<160> 23

<170> FastSEQ for Windows Version 3.0

<210> 1
<211> 4652
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 1

```
tggcactctc cccctgtcg cgttcgctcg ctcgctggct cgtttggggg ggtggcagct      60
caaagagctg ccagacgacg gccctctggc cgtcgccccc ccaaacgagc cagcgagcga     120
gcgaacgcga caggggggag agtgccacac tctcaagcaa gggggttttg taagcagtga     180
tgtcataatg atgtaatgct tattgtcacg cgatagttaa tgattaacag tcatgtgatg     240
tgttttatcc aataggaaga aagcgcgcgt atgagttctc gcgagacttc cggggtataa     300
aagaccgagt gaacgagccc gccgccattc tttgctctgg actgctagag gaccctcgct     360
gccatggcta ccttctatga agtcattgtt cgcgtcccat ttgacgtgga ggaacatctg     420
cctggaattt ctgacagctt tgtggactgg gtaactggtc aaatttggga gctgcctcca     480
gagtcagatt taaatttgac tctggttgaa cagcctcagt tgacggtggc tgatagaatt     540
cgccgcgtgt tcctgtacga gtggaacaaa ttttccaagc aggagtccaa attctttgtg     600
cagtttgaaa agggatctga atattttcat ctgcacacgc ttgtggagac ctccggcatc     660
tcttccatgg tcctcggccg ctacgtgagt cagattcgcg cccagctggt gaaagtggtc     720
ttccagggaa ttgaacccca gatcaacgac tgggtcgcca tcaccaaggt aaagaagggc     780
ggagccaata aggtggtgga ttctgggtat attcccgcct acctgctgcc gaaggtccaa     840
ccggagcttc agtgggcgtg gacaaacctg gacgagtata aattggccgc cctgaatctg     900
gaggagcgca aacggctcgt cgcgcagttt ctggcagaat cctcgcagcg ctcgcaggag     960
gcggcttcgc agcgtgagtt ctcggctgac ccggtcatca aaagcaagac ttcccagaaa    1020
tacatggcgc tcgtcaactg gctcgtggag cacggcatca cttccgagaa gcagtggatc    1080
caggaaaatc aggagagcta cctctccttc aactccaccg gcaactctcg gagccagatc    1140
aaggccgcgc tcgacaacgc gaccaaaatt atgagtctga caaaaagcgc ggtggactac    1200
ctcgtgggga gctccgttcc cgaggacatt tcaaaaaaca gaatctggca aattttttgag    1260
atgaatggct acgacccggc ctacgcggga tccatcctct acggctggtg tcagcgctcc    1320
ttcaacaaga ggaacaccgt ctggctctac ggacccgcca cgaccggcaa gaccaacatc    1380
gcggaggcca tcgcccacac tgtgcccttt tacggctgcg tgaactggac caatgaaaac    1440
tttcccttta atgactgtgt ggacaaaatg ctcatttggt gggaggaggg aaagatgacc    1500
aacaaggtgg ttgaatccgc caaggccatc ctggggggct caaaggtgcg ggtcgatcag    1560
aaatgtaaat cctctgttca aattgattct accctgtca ttgtaacttc caatacaaac    1620
atgtgtgtgg tggtggatgg gaattccacg acctttgaac accagcagcc gctggaggac    1680
```

```
cgcatgttca aatttgaact gactaagcgg ctcccgccag attttggcaa gattactaag   1740
caggaagtca aggacttttt tgcttgggca aaggtcaatc aggtgccggt gactcacgag   1800
tttaaagttc ccagggaatt ggcgggaact aaaggggcgg agaaatctct aaaacgccca   1860
ctgggtgacg tcaccaatac tagctataaa agtctggaga agcgggccag gctctcattt   1920
gttcccgaga cgcctcgcag ttcagacgtg actgttgatc ccgctcctct gcgaccgctc   1980
aattggaatt caaggtatga ttgcaaatgt gactatcatg ctcaatttga caacatttct   2040
aacaaatgtg atgaatgtga atatttgaat cggggcaaaa atggatgtat ctgtcacaat   2100
gtaactcact gtcaaatttg tcatgggatt cccccctggg aaaaggaaaa cttgtcagat   2160
tttggggatt ttgacgatgc caataaagaa cagtaaataa agcgagtagt catgtctttt   2220
gttgatcacc ctccagattg gttggaagaa gttggtgaag gtcttcgcga gttttttgggc   2280
cttgaagcgg gcccaccgaa accaaaaccc aatcagcagc atcaagatca agcccgtggt   2340
cttgtgctgc ctggttataa ctatctcgga cccggaaacg gtctcgatcg aggagagcct   2400
gtcaacaggg cagacgaggt cgcgcgagag cacgacatct cgtacaacga gcagcttgag   2460
gcgggagaca acccctacct caagtacaac cacgcggacg ccgagtttca ggagaagctc   2520
gccgacgaca catccttcgg gggaaacctc ggaaaggcag tctttcaggc caagaaaagg   2580
gttctcgaac ctttttggcct ggttgaagag ggtgctaaga cggcccctac cggaaagcgg   2640
atagacgacc actttccaaa aagaaagaag gctcggaccg aagaggactc caagccttcc   2700
acctcgtcag acgccgaagc tggacccagc ggatcccagc agctgcaaat cccagcccaa   2760
ccagcctcaa gtttgggagc tgatacaatg tctgcgggag gtggcggccc attgggcgac   2820
aataaccaag gtgccgatgg agtgggcaat gcctcgggag attggcattg cgattccacg   2880
tggatggggg acagagtcgt caccaagtcc acccgaacct gggtgctgcc cagctacaac   2940
aaccaccagt accgagagat caaaagcggc tccgtcgacg gaagcaacgc caacgcctac   3000
tttggataca gcacccctg ggggtacttt gactttaacc gcttccacag ccactggagc   3060
ccccgagact ggcaaagact catcaacaac tactggggct tcagaccccg gtccctcaga   3120
gtcaaaatct tcaacattca agtcaaagag gtcacggtgc aggactccac caccaccatc   3180
gccaacaacc tcacctccac cgtccaagtg tttacggacg acgactacca gctgccctac   3240
gtcgtcggca acgggaccga gggatgcctg ccggccttcc ctccgcaggt ctttacgctg   3300
ccgcagtacg gttacgcgac gctgaaccgc gacaacacag aaaatcccac cgagaggagc   3360
agcttcttct gcctagagta ctttcccagc aagatgctga gaacgggcaa caactttgag   3420
tttacctaca cttttgagga ggtgcccttc cactccagct tcgctcccag tcagaacctg   3480
ttcaagctgg ccaacccgct ggtggaccag tacttgtacc gcttcgtgag cacaaataac   3540
actggcggag tccagttcaa caagaacctg gccgggagat acgccaacac ctacaaaaac   3600
tggttcccgg ggcccatggg ccgaacccag ggctggaacc tgggctccgg ggtcaaccgc   3660
gccagtgtca gcgccttcgc cacgaccaat aggatggagc tcgagggcgc gagttaccag   3720
gtgccccgc agccgaacgg catgaccaac aacctccagg gcagcaacac ctatgccctg   3780
gagaacacta tgatcttcaa cagccagccg gcgaacccgg gcaccaccgc cacgtacctc   3840
gagggcaaca tgctcatcac cagcgagagc gagacgcagc cggtgaaccg cgtggcgtac   3900
aacgtcggcg ggcagatggc caccaacaac cagagctcca ccactgcccc cgcgaccggc   3960
acgtacaacc tccaggaaat cgtgcccggc agcgtgtgga tggagaggga cgtgtacctc   4020
caaggaccca tctgggccaa gatcccagag acggggcgc actttcaccc ctctccggcc   4080
atggcggat tcggactcaa acacccaccg cccatgatgc tcatcaagaa cacgcctgtg   4140
cccggaaata tcaccagctt ctcggacgtg ccgtcagca gcttcatcac ccagtacagc   4200
accgggcagg tcaccgtgga tatggagtgg gagctcaaga aggaaaactc caagaggtgg   4260
aacccagaga tccagtacac aaacaactac aacgacccc agtttgtgga cttttgcccg   4320
gacagcaccg gggaatacag aaccaccaga cctatcggaa cccgatacct tacccgaccc   4380
cttttaccca ttcatgtcgc ataccctcaa taaccgtgt attcgtgtca gtaaaatact   4440
gcctcttgtg gtcattcaat gaataacagc ttacaacatc tacaaaacct ccttgcttga   4500
gagtgtggca ctctcccccc tgtcgcgttc gctcgctcgc tggctcgttt ggggggggtgg   4560
cagctcaaag agctgccaga cgacggccct ctggccgtcg cccccccaaa cgagccagcg   4620
agcgagcgaa cgcgacaggg gggagagtgc ca                                  4652
```

<210> 2
<211> 390
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =

synthetic construct

<400> 2

```
Met Ala Leu Val Asn Trp Leu Val Glu His Gly Ile Thr Ser Glu Lys
1               5                   10                  15
Gln Trp Ile Gln Glu Asn Gln Glu Ser Tyr Leu Ser Phe Asn Ser Thr
            20                  25                  30
Gly Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Thr Lys
        35                  40                  45
Ile Met Ser Leu Thr Lys Ser Ala Val Asp Tyr Leu Val Gly Ser Ser
    50                  55                  60
Val Pro Glu Asp Ile Ser Lys Asn Arg Ile Trp Gln Ile Phe Glu Met
65                  70                  75                  80
Asn Gly Tyr Asp Pro Ala Tyr Ala Gly Ser Ile Leu Tyr Gly Trp Cys
                85                  90                  95
Gln Arg Ser Phe Asn Lys Arg Asn Thr Val Trp Leu Tyr Gly Pro Ala
            100                 105                 110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
        115                 120                 125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
    130                 135                 140
Cys Val Asp Lys Met Leu Ile Trp Trp Glu Glu Gly Lys Met Thr Asn
145                 150                 155                 160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                165                 170                 175
Val Asp Gln Lys Cys Lys Ser Ser Val Gln Ile Asp Ser Thr Pro Val
            180                 185                 190
Ile Val Thr Ser Asn Thr Asn Met Cys Val Val Val Asp Gly Asn Ser
    195                 200                 205
Thr Thr Phe Glu His Gln Gln Pro Leu Glu Asp Arg Met Phe Lys Phe
    210                 215                 220
Glu Leu Thr Lys Arg Leu Pro Pro Asp Phe Gly Lys Ile Thr Lys Gln
225                 230                 235                 240
Glu Val Lys Asp Phe Phe Ala Trp Ala Lys Val Asn Gln Val Pro Val
                245                 250                 255
Thr His Glu Phe Lys Val Pro Arg Glu Leu Ala Gly Thr Lys Gly Ala
            260                 265                 270
Glu Lys Ser Leu Lys Arg Pro Leu Gly Asp Val Thr Asn Thr Ser Tyr
    275                 280                 285
Lys Ser Leu Glu Lys Arg Ala Arg Leu Ser Phe Val Pro Glu Thr Pro
    290                 295                 300
Arg Ser Ser Asp Val Thr Val Asp Pro Ala Pro Leu Arg Pro Leu Asn
305                 310                 315                 320
Trp Asn Ser Arg Tyr Asp Cys Lys Cys Asp Tyr His Ala Gln Phe Asp
                325                 330                 335
Asn Ile Ser Asn Lys Cys Asp Glu Cys Glu Tyr Leu Asn Arg Gly Lys
            340                 345                 350
Asn Gly Cys Ile Cys His Asn Val Thr His Cys Gln Ile Cys His Gly
        355                 360                 365
Ile Pro Pro Trp Glu Lys Glu Asn Leu Ser Asp Phe Gly Asp Phe Asp
    370                 375                 380
Asp Ala Asn Lys Glu Gln
385                 390
```

<210> 3
<211> 610
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
      synthetic construct

<400> 3

```
Met Ala Thr Phe Tyr Glu Val Ile Val Arg Val Pro Phe Asp Val Glu
1               5                   10                  15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asp Trp Val Thr Gly
            20                  25                  30
Gln Ile Trp Glu Leu Pro Pro Glu Ser Asp Leu Asn Leu Thr Leu Val
        35                  40                  45
Glu Gln Pro Gln Leu Thr Val Ala Asp Arg Ile Arg Arg Val Phe Leu
    50                  55                  60
Tyr Glu Trp Asn Lys Phe Ser Lys Gln Glu Ser Lys Phe Phe Val Gln
65                  70                  75                  80
Phe Glu Lys Gly Ser Glu Tyr Phe His Leu His Thr Leu Val Glu Thr
            85                  90                  95
Ser Gly Ile Ser Ser Met Val Leu Gly Arg Tyr Val Ser Gln Ile Arg
            100                 105                 110
Ala Gln Leu Val Lys Val Val Phe Gln Gly Ile Glu Pro Gln Ile Asn
        115                 120                 125
Asp Trp Val Ala Ile Thr Lys Val Lys Lys Gly Gly Ala Asn Lys Val
        130                 135                 140
Val Asp Ser Gly Tyr Ile Pro Ala Tyr Leu Leu Pro Lys Val Gln Pro
145                 150                 155                 160
Glu Leu Gln Trp Ala Trp Thr Asn Leu Asp Glu Tyr Lys Leu Ala Ala
                165                 170                 175
Leu Asn Leu Glu Glu Arg Lys Arg Leu Val Ala Gln Phe Leu Ala Glu
            180                 185                 190
Ser Ser Gln Arg Ser Gln Glu Ala Ala Ser Gln Arg Glu Phe Ser Ala
        195                 200                 205
Asp Pro Val Ile Lys Ser Lys Thr Ser Gln Lys Tyr Met Ala Leu Val
    210                 215                 220
Asn Trp Leu Val Glu His Gly Ile Thr Ser Glu Lys Gln Trp Ile Gln
225                 230                 235                 240
Glu Asn Gln Glu Ser Tyr Leu Ser Phe Asn Ser Thr Gly Asn Ser Arg
                245                 250                 255
Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Thr Lys Ile Met Ser Leu
        260                 265                 270
Thr Lys Ser Ala Val Asp Tyr Leu Val Gly Ser Ser Val Pro Glu Asp
    275                 280                 285
Ile Ser Lys Asn Arg Ile Trp Gln Ile Phe Glu Met Asn Gly Tyr Asp
    290                 295                 300
Pro Ala Tyr Ala Gly Ser Ile Leu Tyr Gly Trp Cys Gln Arg Ser Phe
305                 310                 315                 320
Asn Lys Arg Asn Thr Val Trp Leu Tyr Gly Pro Ala Thr Thr Gly Lys
                325                 330                 335
Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro Phe Tyr Gly Cys
            340                 345                 350
Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp Cys Val Asp Lys
            355                 360                 365
Met Leu Ile Trp Trp Glu Glu Gly Lys Met Thr Asn Lys Val Val Glu
    370                 375                 380
Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg Val Asp Gln Lys
385                 390                 395                 400
Cys Lys Ser Ser Val Gln Ile Asp Ser Thr Pro Val Ile Val Thr Ser
                405                 410                 415
```

Asn Thr Asn Met Cys Val Val Val Asp Gly Asn Ser Thr Thr Phe Glu
420   425   430

His Gln Gln Pro Leu Glu Asp Arg Met Phe Lys Phe Glu Leu Thr Lys
435   440   445

Arg Leu Pro Pro Asp Phe Gly Lys Ile Thr Lys Gln Glu Val Lys Asp
450   455   460

Phe Phe Ala Trp Ala Lys Val Asn Gln Val Pro Val Thr His Glu Phe
465   470   475   480

Lys Val Pro Arg Glu Leu Ala Gly Thr Lys Gly Ala Glu Lys Ser Leu
485   490   495

Lys Arg Pro Leu Gly Asp Val Thr Asn Thr Ser Tyr Lys Ser Leu Glu
500   505   510

Lys Arg Ala Arg Leu Ser Phe Val Pro Glu Thr Pro Arg Ser Ser Asp
515   520   525

Val Thr Val Asp Pro Ala Pro Leu Arg Pro Leu Asn Trp Asn Ser Arg
530   535   540

Tyr Asp Cys Lys Cys Asp Tyr His Ala Gln Phe Asp Asn Ile Ser Asn
545   550   555   560

Lys Cys Asp Glu Cys Glu Tyr Leu Asn Arg Gly Lys Asn Gly Cys Ile
565   570   575

Cys His Asn Val Thr His Cys Gln Ile Cys His Gly Ile Pro Pro Trp
580   585   590

Glu Lys Glu Asn Leu Ser Asp Phe Gly Asp Phe Asp Asp Ala Asn Lys
595   600   605

Glu Gln
610

          <210> 4
          <211> 724
          <212> PRT
          <213> Artificial Sequence

          <220>
          <223> Description of Artificial Sequence:/Note =
                synthetic construct

          <400> 4
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1   5   10   15
Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
            20   25   30
Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
        35   40   45
Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
    50   55   60
Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65   70   75   80
Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85   90   95
Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100   105   110
Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115   120   125
Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130   135   140
Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145   150   155   160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                    165   170   175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
                180   185   190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195   200   205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210   215   220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225   230   235   240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245   250   255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260   265   270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275   280   285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290   295   300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305   310   315   320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325   330   335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340   345   350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355   360   365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370   375   380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385   390   395   400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405   410   415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420   425   430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435   440   445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450   455   460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465   470   475   480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485   490   495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500   505   510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515   520   525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
        530   535   540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545   550   555   560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565   570   575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580   585   590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
            595   600   605

```
Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610             615             620
Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625             630             635             640
Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
            645             650             655
Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
            660             665             670
Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
        675             680             685
Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
    690             695             700
Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705             710             715             720
Thr Arg Pro Leu
```

<210> 5
<211> 588
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
      synthetic construct

```
<400> 5
Thr Ala Pro Thr Gly Lys Arg Ile Asp Asp His Phe Pro Lys Arg Lys
  1             5               10              15
Lys Ala Arg Thr Glu Glu Asp Ser Lys Pro Ser Thr Ser Ser Asp Ala
            20              25              30
Glu Ala Gly Pro Ser Gly Ser Gln Gln Leu Gln Ile Pro Ala Gln Pro
        35              40              45
Ala Ser Ser Leu Gly Ala Asp Thr Met Ser Ala Gly Gly Gly Gly Pro
    50              55              60
Leu Gly Asp Asn Asn Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly
65              70              75              80
Asp Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Val Thr Lys
            85              90              95
Ser Thr Arg Thr Trp Val Leu Pro Ser Tyr Asn Asn His Gln Tyr Arg
            100             105             110
Glu Ile Lys Ser Gly Ser Val Asp Gly Ser Asn Ala Asn Ala Tyr Phe
        115             120             125
Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Ser
    130             135             140
His Trp Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Tyr Trp Gly
145             150             155             160
Phe Arg Pro Arg Ser Leu Arg Val Lys Ile Phe Asn Ile Gln Val Lys
            165             170             175
Glu Val Thr Val Gln Asp Ser Thr Thr Thr Ile Ala Asn Asn Leu Thr
        180             185             190
Ser Thr Val Gln Val Phe Thr Asp Asp Asp Tyr Gln Leu Pro Tyr Val
    195             200             205
Val Gly Asn Gly Thr Glu Gly Cys Leu Pro Ala Phe Pro Pro Gln Val
210             215             220
Phe Thr Leu Pro Gln Tyr Gly Tyr Ala Thr Leu Asn Arg Asp Asn Thr
225             230             235             240
```

Glu Asn Pro Thr Glu Arg Ser Ser Phe Phe Cys Leu Glu Tyr Phe Pro
                245   250   255
Ser Lys Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Thr Tyr Asn Phe
            260   265   270

Glu Glu Val Pro Phe His Ser Ser Phe Ala Pro Ser Gln Asn Leu Phe
            275   280   285
Lys Leu Ala Asn Pro Leu Val Asp Gln Tyr Leu Tyr Arg Phe Val Ser
        290   295   300
Thr Asn Asn Thr Gly Gly Val Gln Phe Asn Lys Asn Leu Ala Gly Arg
305   310   315   320
Tyr Ala Asn Thr Tyr Lys Asn Trp Phe Pro Gly Pro Met Gly Arg Thr
                325   330   335
Gln Gly Trp Asn Leu Gly Ser Gly Val Asn Arg Ala Ser Val Ser Ala
            340   345   350
Phe Ala Thr Thr Asn Arg Met Glu Leu Glu Gly Ala Ser Tyr Gln Val
            355   360   365
Pro Pro Gln Pro Asn Gly Met Thr Asn Asn Leu Gln Gly Ser Asn Thr
        370   375   380
Tyr Ala Leu Glu Asn Thr Met Ile Phe Asn Ser Gln Pro Ala Asn Pro
385   390   395   400
Gly Thr Thr Ala Thr Tyr Leu Glu Gly Asn Met Leu Ile Thr Ser Glu
                405   410   415
Ser Glu Thr Gln Pro Val Asn Arg Val Ala Tyr Asn Val Gly Gly Gln
            420   425   430
Met Ala Thr Asn Asn Gln Ser Ser Thr Thr Ala Pro Ala Thr Gly Thr
            435   440   445
Tyr Asn Leu Gln Glu Ile Val Pro Gly Ser Val Trp Met Glu Arg Asp
        450   455   460
Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro Glu Thr Gly Ala
465   470   475   480
His Phe His Pro Ser Pro Ala Met Gly Gly Phe Gly Leu Lys His Pro
                485   490   495
Pro Pro Met Met Leu Ile Lys Asn Thr Pro Val Pro Gly Asn Ile Thr
            500   505   510
Ser Phe Ser Asp Val Pro Val Ser Ser Phe Ile Thr Gln Tyr Ser Thr
        515   520   525
Gly Gln Val Thr Val Glu Met Glu Trp Glu Leu Lys Lys Glu Asn Ser
        530   535   540
Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Asn Asn Tyr Asn Asp Pro
545   550   555   560
Gln Phe Val Asp Phe Ala Pro Asp Ser Thr Gly Glu Tyr Arg Thr Thr
                565   570   575
Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
            580   585

        <210> 6
        <211> 532
        <212> PRT
        <213> Artificial Sequence

        <220>
        <223> Description of Artificial Sequence:/Note =
             synthetic construct

        <400> 6
    Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
    1   5   10   15

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
         20   25   30

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
       35   40   45

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
      50   55   60

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
65   70   75   80

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
         85   90   95

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
       100   105   110

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
       115   120   125

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
       130   135   140

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
145   150   155   160

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
         165   170   175

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
       180   185   190

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
       195   200   205

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
       210   215   220

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
225   230   235   240

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
         245   250   255

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
       260   265   270

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
       275   280   285

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
       290   295   300

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
305   310   315   320

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
         325   330   335

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
       340   345   350

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
       355   360   365

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
       370   375   380

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
385   390   395   400

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
         405   410   415

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
       420   425   430

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
       435   440   445

Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
       450   455   460

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
465   470   475   480
Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
                485   490   495
Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
            500   505   510
Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
        515   520   525
Thr Arg Pro Leu
    530

<210> 7
<211> 2307
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
      synthetic construct

<400> 7
aggctctcat ttgttcccga gacgcctcgc agttcagacg tgactgttga tcccgctcct   60
ctgcgaccgc tcaattggaa ttcaagtaaa taaagcgagt agtcatgtct tttgttgatc   120
accctccaga ttggttggaa gaagttggtg aaggtcttcg cgagtttttg ggccttgaag   180
cgggcccacc gaaaccaaaa cccaatcagc agcatcaaga tcaagcccgt ggtcttgtgc   240
tgcctggtta taactatctc ggacccggaa acggtctcga tcgaggagag cctgtcaaca   300
gggcagacga ggtcgcgcga gagcacgaca tctcgtacaa cgagcagctt gaggcgggag   360
acaacccta cctcaagtac aaccacgcgg acgccgagtt tcaggagaag ctcgccgacg   420
acacatcctt cgggggaaac ctcggaaagg cagtctttca ggccaagaaa agggttctcg   480
aacctttggg cctggttgaa gagggtgcta agacggcccc taccggaaag cggatagacg   540
accactttcc aaaaagaaag aaggctcgga ccgaagagga ctccaagcct tccacctcgt   600
cagacgccga agctggaccc agcggatccc agcagctgca aatcccagcc caaccagcct   660
caagtttggg agctgataca atgtctgcgg gaggtggcgg cccattgggc gacaataacc   720
aaggtgccga tggagtgggc aatgcctcgg gagattggca ttgcgattcc acgtggatgg   780
gggacagagt cgtcaccaag tccacccgaa cctgggtgct gcccagctac aacaaccacc   840
agtaccgaga gatcaaaagc ggctccgtcg acggaagcaa cgccaacgcc tactttggat   900
acagcacccc ctggggggtac tttgacttta accgcttcca cagccactgg agcccccgag   960
actggcaaag actcatcaac aactactggg gcttcagacc ccggtccctc agagtcaaaa   1020
tcttcaacat tcaagtcaaa gaggtcacgg tgcaggactc caccaccacc atcgccaaca   1080
acctcacctc caccgtccaa gtgtttacgg acgacgacta ccagctgccc tacgtcgtcg   1140
gcaacgggac cgagggatgc ctgccggcct tccctccgca ggtctttacg ctgccgcagt   1200
acggttacgc gacgctgaac cgcgacaaca cagaaaatcc caccgagagg agcagcttct   1260
tctgcctaga gtactttccc agcaagatgc tgagaacggg caacaacttt gagtttacct   1320
acaactttga ggaggtgccc ttccactcca gcttcgctcc cagtcagaac ctgttcaagc   1380
tggccaaccc gctggtggac cagtacttgt accgcttcgt gagcctacaa aactggttcc   1440
gagtccagtt caacaagaac ctggccggga gatacgccaa cacctacaaa aactggttcc   1500
cggggcccat gggccgaacc cagggctgga acctgggctc cggggtcaac cgcgccagtg   1560
tcagcgcctt cgccacgacc aataggatgg agctcgaggg cgcgagttac caggtgcccc   1620
cgcagccgaa cggcatgacc aacaacctcc agggcagcaa cacctatgcc ctggagaaca   1680
ctatgatctt caacagccag ccggcgaacc cgggcaccac cgccacgtac ctcgagggca   1740
acatgctcat caccagcgag agcgagacgc agccggtgaa ccgcgtggcg tacaacgtcg   1800
gcgggcagat ggccaccaac aaccagagct ccaccactgc ccccgcgacc ggcacgtaca   1860
acctccagga aatcgtgccc ggcagcgtgt ggatggagag ggacgtgtac ctccaaggac   1920
ccatctgggc caagatccca gagacggggg cgcactttca ccctctccg gccatgggcg   1980
gattcggact caaacaccca ccgcccatga tgctcatcaa gaacacgcct gtgcccggaa   2040
atatcaccag cttctcggac gtgcccgtca gcagcttcat cacccagtac agcaccgggc   2100
aggtcaccgt ggagatggag tgggagctca agaaggaaaa ctccaagagg tggaacccag   2160
agatccagta cacaaacaac tacaacgacc cccagtttgt ggactttgcc ccggacagca   2220

ccggggaata cagaaccacc agacctatcg gaacccgata ccttacccga cccctttaac   2280
ccattcatgt cgcataccct caataaa   2307

<210> 8
<211> 2264
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
     synthetic construct

<400> 8
aggctctcat ttgttcccga gacgcctcgc agttcagacg tgactgttga tcccgctcct   60
ctgcgaccgc tcaattggaa ttcaagattg gttggaagaa gttggtgaag gtcttcgcga   120
gtttttgggc cttgaagcgg gcccaccgaa accaaaaccc aatcagcagc atcaagatca   180
agcccgtggt cttgtgctgc ctggttataa ctatctcgga cccggaaacg gtctcgatcg   240
aggagagcct gtcaacaggg cagacgaggt cgcgcgagag cacgacatct cgtacaacga   300
gcagcttgag gcgggagaca acccctacct caagtacaac cacgcggacg ccgagtttca   360
ggagaagctc gccgacgaca catccttcgg gggaaacctc ggaaaggcag tctttcaggc   420
caagaaaagg gttctcgaac cttttggcct ggttgaagag ggtgctaaga cggcccctac   480
cggaaagcgg atagacgacc actttccaaa aagaaagaag gctcggaccg aagaggactc   540
caagccttcc acctcgtcag acgccgaagc tggacccagc ggatcccagc agctgcaaat   600
cccagcccaa ccagcctcaa gtttgggagc tgatacaatg tctgcgggag gtggcggccc   660
attgggcgac aataaccaag gtgccgatgg agtgggcaat gcctcgggag attggcattg   720
cgattccacg tggatggggg acagagtcgt caccaagtcc acccgaacct gggtgctgcc   780
cagctacaac aaccaccagt accgagagat caaaagcggc tccgtcgacg gaagcaacgc   840
caacgcctac tttggataca gcaccccctg ggggtacttt gactttaacc gcttccacag   900
ccactggagc ccccgagact ggcaaagact catcaacaac tactggggct tcagaccccg   960
gtccctcaga gtcaaaatct tcaacattca agtcaaagag gtcacggtgc aggactccac   1020
caccaccatc gccaacaacc tcacctccac cgtccaagtg tttacggacg acgactacca   1080
gctgccctac gtcgtcggca acgggaccga gggatgcctg ccggccttcc ctccgcaggt   1140
ctttacgctg ccgcagtacg gttacgcgac gctgaaccgc gacaacacag aaaatcccac   1200
cgagaggagc agcttcttct gcctagagta ctttcccagc aagatgctga gaacgggcaa   1260
caactttgag tttacctaca actttgagga ggtgcccttc cactccagct tcgctcccag   1320
tcagaacctg ttcaagctgg ccaacccgct ggtggaccag tacttgtacc gcttcgtgag   1380
cacaaataac actggcggag tccagttcaa caagaacctg gccgggagat acgccaacac   1440
ctacaaaaac tggttcccgg ggcccatggg ccgaacccag ggctggaacc tgggctccgg   1500
ggtcaaccgc gccagtgtca gcgccttcgc cacgaccaat aggatggagc tcgagggcgc   1560
gagttaccag gtgccccgc agccgaacgg catgaccaac aacctccagg gcagcaacac   1620
ctatgccctg gagaacacta tgatcttcaa cagccagccg gcgaacccgg gcaccaccgc   1680
cacgtacctc gagggcaaca tgctcatcac cagcgagagc gagacgcagc cggtgaaccg   1740
cgtggcgtac aacgtcggcg ggcagatggc caccaacaac cagagctcca ccactgcccc   1800
cgcgaccggc acgtacaacc tccaggaaat cgtgcccggc agcgtgtgga tggagaggga   1860
cgtgtacctc caaggaccca tctgggccaa gatcccagag acggggcgc actttcaccc   1920
ctctccggcc atgggcggat cggactcaa acacccaccg cccatgatgc tcatcaagaa   1980
cacgcctgtg cccggaaata tcaccagctt ctcggacgtg cccgtcagca gcttcatcac   2040
ccagtacagc accgggcagg tcaccgtgga gatggagtgg gagctcaaga aggaaaactc   2100
caagaggtgg aacccagaga tccagtacac aaacaactac aacgaccccc agtttgtgga   2160
ctttgccccg gacagcaccg gggaatacag aaccaccaga cctatcggaa cccgataccc   2220
tacccgaccc ctttaaccca ttcatgtcgc ataccctcaa taaa   2264

<210> 9
<211> 2264
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/Note =
      synthetic construct

<400> 9

```
aggctctcat ttgttcccga gacgcctcgc agttcagacg tgactgttga tcccgctcct    60
ctgcgaccgc tcaattggaa ttcaagattg gttggaagaa gttggtgaag gtcttcgcga   120
gtttttgggc cttgaagcgg gcccaccgaa accaaaaccc aatcagcagc atcaagatca   180
agcccgtggt cttgtgctgc ctggttataa ctatctcgga cccggaaacg gtctcgatcg   240
aggagagcct gtcaacaggg cagaccctacct cgcgcgagag cacgacatct cgtacaacga   300
gcagcttgag gcgggagaca acccctacct caagtacaac cacgcggacg ccgagtttca   360
ggagaagctc gccgacgaca catccttcgg gggaaacctc ggaaaggcag tctttcaggc   420
caagaaaagg gttctcgaac cttttggcct ggttgaagag ggtgctaaga cggcccctac   480
cggaaagcgg atagacgacc actttccaaa aagaaagaag gctcggaccg aagaggactc   540
caagccttcc acctcgtcag acgccgaagc tggacccagc ggatcccagc agctgcaaat   600
cccagcccaa ccagcctcaa gtttgggagc tgatacaatg tctgcgggag gtggcggccc   660
attgggcgac aataaccaag gtgccgatgg agtgggcaat gcctcgggag attggcattg   720
cgattccacg tggatggggg acagagtcgt caccaagtcc acccgaacct gggtgctgcc   780
cagctacaac aaccaccagt accgagagat caaaagcggc tccgtcgacg gaagcaacgc   840
caacgcctac tttggataca gcacccccctg ggggtacttt gactttaacc gcttccacag   900
ccactggagc ccccgagact ggcaaagact catcaacaac tactggggct tcagaccccg   960
gtccctcaga gtcaaaatct tcaacattca agtcaaagag gtcacggtgc aggactccac  1020
caccaccatc gccaacaacc tcacctccac cgtccaagtg tttacggacg acgactacca  1080
gctgccctac gtcgtcggca acgggaccga gggatgcctg ccggccttcc ctccgcaggt  1140
ctttacgctg ccgcagtacg gttacgcgac gctgaaccgc gacaacacag aaaatcccac  1200
cgagaggagc agcttcttct gcctagagta ctttcccagc aagatgctga gaacgggcaa  1260
caactttgag tttacctaca actttgagga ggtgcccttc cactccagct tcgctcccag  1320
tcagaacctg ttcaagctgg ccaacccgct ggtggaccag tacttgtacc gcttcgtgag  1380
cacaaataac actggcggag tccagttcaa caagaacctg gccgggagat acgccaacac  1440
ctacaaaaac tggttcccgg ggcccatggg ccgaacccag ggctggaacc tgggctccgg  1500
ggtcaaccgc gccagtgtca gcgccttcgc cacgaccaat aggatggagc tcgagggcgc  1560
gagttaccag gtgcccccgc agccgaacgg catgaccaac aacctccagg gcagcaacac  1620
ctatgccctg gagaacacta tgatcttcaa cagccagccg gcgaacccgg gcaccaccgc  1680
cacgtacctc gagggcaaca tgctcatcac cagcgagagc gagacgcagc cggtgaaccg  1740
cgtggcgtac aacgtcggcg ggcagatggc caccaacaac cagagctcca ccactgcccc  1800
cgcgaccggc acgtacaacc tccaggaaat cgtgcccggc agcgtgtgga tggagaggga  1860
cgtgtacctc caaggaccca tctgggccaa gatcccagag acggggcgc actttcaccc  1920
ctctccggcc atgggcggat tcggactcaa acacccaccg cccatgatgc tcatcaagaa  1980
cacgcctgtg cccggaaata tcaccagctt ctcggacgtg cccgtcagca gcttcatcac  2040
ccagtacagc accgggcagg tcaccgtgga gatggagtgg gagctcaaga aggaaaactc  2100
caagaggtgg aacccagaga tccagtacac aaacaactac aacgaccccc agtttgtgga  2160
ctttgccccg gacagcaccg gggaatacag aaccaccaga cctatcggaa cccgatacct  2220
tacccgaccc ctttaaccca ttcatgtcgc ataccctcaa taaa                     2264
```

<210> 10
<211> 1292
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
      synthetic construct

<400> 10

```
agcgcaaacg gctcgtcgcg cagtttctgg cagaatcctc gcagcgctcg caggaggcgg    60
cttcgcagcg tgagttctcg gctgacccgg tcatcaaaag caagacttcc cagaaataca   120
tggcgctcgt caactggctc gtggagcacg gcatcacttc cgagaagcag tggatccagg   180
aaaatcagga gagctacctc tccttcaact ccaccggcaa ctctcggagc cagatcaagg   240
ccgcgctcga caacgcgacc aaaattatga gtctgacaaa aagcgcggtg gactacctcg   300
```

```
tggggagctc cgttcccgag gacatttcaa aaaacagaat ctggcaaatt tttgagatga    360
atggctacga cccggcctac gcgggatcca tcctctacgg ctggtgtcag cgctccttca    420
acaagaggaa caccgtctgg ctctacggac ccgccacgac cggcaagacc aacatcgcgg    480
aggccatcgc ccacactgtg cccttttacg gctgcgtgaa ctggaccaat gaaaactttc    540
cctttaatga ctgtgtggac aaaatgctca tttggtggga ggagggaaag atgaccaaca    600
aggtggttga atccgccaag gccatcctgg ggggctcaaa ggtgcgggtc gatcagaaat    660
gtaaatcctc tgttcaaatt gattctaccc ctgtcattgt aacttccaat acaaacatgt    720
gtgtggtggt ggatgggaat tccacgacct ttgaacacca gcagccgctg gaggaccgca    780
tgttcaaatt tgaactgact aagcggctcc cgccagattt tggcaagatt actaagcagg    840
aagtcaagga cttttttgct tgggcaaagg tcaatcaggt gccggtgact cacgagttta    900
aagttcccag ggaattggcg ggaactaaag gggcggagaa atctctaaaa cgcccactgg    960
gtgacgtcac caatactagc tataaaagtc tggagaagcg ggccaggctc tcatttgttc   1020
ccgagacgcc tcgcagttca gacgtgactg ttgatcccgc tcctctgcga ccgctcaatt   1080
ggaattcaag gtatgattgc aaatgtgact atcatgctca atttgacaac atttctaaca   1140
aatgtgatga atgtgaatat ttgaatcggg gcaaaaatgg atgtatctgt cacaatgtaa   1200
ctcactgtca aatttgtcat gggattcccc cctgggaaaa ggaaaacttg tcagattttg   1260
gggattttga cgatgccaat aaagaacagt aa                                 1292
```

<210> 11
<211> 1870
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
      synthetic construct

<400> 11

```
attctttgct ctggactgct agaggaccct cgctgccatg gctaccttct atgaagtcat     60
tgttcgcgtc ccatttgacg tggaggaaca tctgcctgga atttctgaca gctttgtgga    120
ctgggtaact ggtcaaattt gggagctgcc tccagagtca gatttaaatt tgactctggt    180
tgaacagcct cagttgacgg tggctgatag aattcgccgc gtgttcctgt acgagtggaa    240
caaattttcc aagcaggagt ccaaattctt tgtgcagttt gaaaagggat ctgaatattt    300
tcatctgcac acgcttgtgg agacctccgg catctcttcc atggtcctcg gccgctacgt    360
gagtcagatt cgcgcccagc tggtgaaagt ggtcttccag ggaattgaac cccagatcaa    420
cgactgggtc gccatcacca aggtaaagaa gggcggagcc aataaggtgg tggattctgg    480
gtatattccc gcctacctgc tgccgaaggt ccaaccggag cttcagtggg cgtggacaaa    540
cctggacgag tataaattgg ccgccctgaa tctggaggag cgcaaacggc tcgtcgcgca    600
gtttctggca gaatcctcgc agcgctcgca ggaggcggct tcgcagcgtg agttctcggc    660
tgacccggtc atcaaaagca agacttccca gaaatacatg gcgctcgtca actggctcgt    720
ggagcacggc atcacttccg agaagcagtg gatccaggaa aatcaggaga gctacctctc    780
cttcaactcc accggcaact ctcggagcca gatcaaggcc gcgctcgaca acgcgaccaa    840
aattatgagt ctgacaaaaa gcgcggtgga ctacctcgtg gggagctccg ttcccgagga    900
catttcaaaa aacagaatct ggcaaatttt tgagatgaat ggctacgacc cggcctacgc    960
gggatccatc tctacggct ggtgtcagcg ctccttcaac aagaggaacc cgtctggct   1020
ctacggaccc gccacgaccg gcaagaccaa catcgcggag gccatcgccc acactgtgcc   1080
ctttttacggc tgcgtgaact ggaccaatga aaactttccc tttaatgact gtgtggacaa   1140
aatgctcatt tggtgggagg agggaaagat gaccaacaag gtggttgaat ccgccaaggc   1200
catcctgggg ggctcaaagg tgcgggtcga tcagaaatgt aaatcctctg ttcaaattga   1260
ttctacccct gtcattgtaa cttccaatac aaacatgtgt gtggtggtgg atgggaattc   1320
cacgaccttt gaacaccagc agccgctgga ggaccgcatg ttcaaatttg aactgactaa   1380
gcggctcccg ccagattttg caagattac taagcaggaa gtcaaggact tttttgcttg   1440
ggcaaaggtc aatcaggtgc cggtgactca cgagtttaaa gttcccaggg aattggcggg   1500
aactaaaggg gcggagaaat ctctaaaacg cccactgggt gacgtcacca atactagcta   1560
taaaagtctg gagaagcggg ccaggctctc atttgttccc gagacgcctc gcagttcaga   1620
cgtgactgtt gatcccgctc ctctgcgacc gctcaattgg aattcaaggt atgattgcaa   1680
atgtgactat catgctcaat ttgacaacat ttctaacaaa tgtgatgaat gtgaatattt   1740
gaatcggggc aaaaatggat gtatctgtca caatgtaact cactgtcaaa tttgtcatgg   1800
```

gattcccccc tgggaaaagg aaaacttgtc agattttggg gattttgacg atgccaataa   1860
agaacagtaa   1870

<210> 12
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
      synthetic construct

<400> 12

```
Met Ala Leu Val Asn Trp Leu Val Glu His Gly Ile Thr Ser Glu Lys
1               5                   10                  15
Gln Trp Ile Gln Glu Asn Gln Glu Ser Tyr Leu Ser Phe Asn Ser Thr
            20                  25                  30
Gly Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Thr Lys
        35                  40                  45
Ile Met Ser Leu Thr Lys Ser Ala Val Asp Tyr Leu Val Gly Ser Ser
    50                  55                  60
Val Pro Glu Asp Ile Ser Lys Asn Arg Ile Trp Gln Ile Phe Glu Met
65                  70                  75                  80
Asn Gly Tyr Asp Pro Ala Tyr Ala Gly Ser Ile Leu Tyr Gly Trp Cys
                85                  90                  95
Gln Arg Ser Phe Asn Lys Arg Asn Thr Val Trp Leu Tyr Gly Pro Ala
            100                 105                 110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
            115                 120                 125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
    130                 135                 140
Cys Val Asp Lys Met Leu Ile Trp Trp Glu Glu Gly Lys Met Thr Asn
145                 150                 155                 160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                165                 170                 175
Val Asp Gln Lys Cys Lys Ser Ser Val Gln Ile Asp Ser Thr Pro Val
            180                 185                 190
Ile Val Thr Ser Asn Thr Asn Met Cys Val Val Val Asp Gly Asn Ser
        195                 200                 205
Thr Thr Phe Glu His Gln Gln Pro Leu Glu Asp Arg Met Phe Lys Phe
    210                 215                 220
Glu Leu Thr Lys Arg Leu Pro Pro Asp Phe Gly Lys Ile Thr Lys Gln
225                 230                 235                 240
Glu Val Lys Asp Phe Phe Ala Trp Ala Lys Val Asn Gln Val Pro Val
                245                 250                 255
Thr His Glu Phe Lys Val Pro Arg Glu Leu Ala Gly Thr Lys Gly Ala
            260                 265                 270
Glu Lys Ser Leu Lys Arg Pro Leu Gly Asp Val Thr Asn Thr Ser Tyr
        275                 280                 285
Lys Ser Leu Glu Lys Arg Ala Arg Leu Ser Phe Val Pro Glu Thr Pro
    290                 295                 300
Arg Ser Ser Asp Val Thr Val Asp Pro Ala Pro Leu Arg Pro Leu Asn
305                 310                 315                 320
Trp Asn Ser Arg Leu Val Gly Arg Ser Trp
                325                 330
```

<210> 13
<211> 1115

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
      synthetic construct

<400> 13

```
aggagcgcaa acggctcgtc gcgcagtttc tggcagaatc ctcgcagcgc tcgcaggagg      60
cggcttcgca gcgtgagttc tcggctgacc cggtcatcaa aagcaagact tcccagaaat     120
acatggcgct cgtcaactgg ctcgtggagc acggcatcac ttccgagaag cagtggatcc     180
aggaaaatca ggagagctac ctctccttca actccaccgg caactctcgg agccagatca     240
aggccgcgct cgacaacgcg accaaaatta tgagtctgac aaaaagcgcg gtggactacc     300
tcgtggggag ctccgttccc gaggacattt caaaaaacag aatctggcaa attttttgaga     360
tgaatggcta cgacccggcc tacgcgggat ccatcctcta cggctggtgt cagcgctcct     420
tcaacaagag gaacaccgtc tggctctacg acccgccac gaccggcaag accaacatcg     480
cggaggccat cgcccacact gtgcccttt acggctgcgt gaactggacc aatgaaaact     540
ttccctttaa tgactgtgtg gacaaaatgc tcatttggtg ggaggaggga aagatgacca     600
acaaggtggt tgaatccgcc aaggccatcc tggggggctc aaaggtgcgg gtcgatcaga     660
aatgtaaatc ctctgttcaa attgattcta ccctgtcat tgtaacttcc aatacaaaca     720
tgtgtgtggt ggtggatggg aattccacga cctttgaaca ccagcagccg ctggaggacc     780
gcatgttcaa atttgaactg actaagcggc tcccgccaga ttttggcaag attactaagc     840
aggaagtcaa ggacttttt gcttgggcaa aggtcaatca ggtgccggtg actcacgagt     900
ttaaagttcc cagggaattg gcgggaacta aaggggcgga gaaatctcta aaacgcccac     960
tgggtgacgt caccaatact agctataaaa gtctggagaa gcgggccagg ctctcatttg    1020
ttcccgagac gcctcgcagt tcagacgtga ctgttgatcc cgctcctctg cgaccgctca    1080
attggaattc aagattggtt ggaagaagtt ggtga                              1115
```

<210> 14
<211> 550
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
      synthetic construct

<400> 14

```
Met Ala Thr Phe Tyr Glu Val Ile Val Arg Val Pro Phe Asp Val Glu
1               5                  10                  15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asp Trp Val Thr Gly
                20                  25                  30
Gln Ile Trp Glu Leu Pro Pro Glu Ser Asp Leu Asn Leu Thr Leu Val
            35                  40                  45
Glu Gln Pro Gln Leu Thr Val Ala Asp Arg Ile Arg Arg Val Phe Leu
        50                  55                  60
Tyr Glu Trp Asn Lys Phe Ser Lys Gln Glu Ser Lys Phe Phe Val Gln
65                  70                  75                  80
Phe Glu Lys Gly Ser Glu Tyr Phe His Leu His Thr Leu Val Glu Thr
                85                  90                  95
Ser Gly Ile Ser Ser Met Val Leu Gly Arg Tyr Val Ser Gln Ile Arg
            100                 105                 110
Ala Gln Leu Val Lys Val Val Phe Gln Gly Ile Glu Pro Gln Ile Asn
        115                 120                 125
Asp Trp Val Ala Ile Thr Lys Val Lys Lys Gly Gly Ala Asn Lys Val
    130                 135                 140
Val Asp Ser Gly Tyr Ile Pro Ala Tyr Leu Leu Pro Lys Val Gln Pro
145                 150                 155                 160
```

Glu Leu Gln Trp Ala Trp Thr Asn Leu Asp Glu Tyr Lys Leu Ala Ala
                 165   170   175

Leu Asn Leu Glu Glu Arg Lys Arg Leu Val Ala Gln Phe Leu Ala Glu
            180   185   190

Ser Ser Gln Arg Ser Gln Glu Ala Ala Ser Gln Arg Glu Phe Ser Ala
            195   200   205

Asp Pro Val Ile Lys Ser Lys Thr Ser Gln Lys Tyr Met Ala Leu Val
  210   215   220

Asn Trp Leu Val Glu His Gly Ile Thr Ser Glu Lys Gln Trp Ile Gln
225   230   235   240

Glu Asn Gln Glu Ser Tyr Leu Ser Phe Asn Ser Thr Gly Asn Ser Arg
            245   250   255

Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Thr Lys Ile Met Ser Leu
            260   265   270

Thr Lys Ser Ala Val Asp Tyr Leu Val Gly Ser Ser Val Pro Glu Asp
            275   280   285

Ile Ser Lys Asn Arg Ile Trp Gln Ile Phe Glu Met Asn Gly Tyr Asp
  290   295   300

Pro Ala Tyr Ala Gly Ser Ile Leu Tyr Gly Trp Cys Gln Arg Ser Phe
305   310   315   320

Asn Lys Arg Asn Thr Val Trp Leu Tyr Gly Pro Ala Thr Thr Gly Lys
            325   330   335

Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro Phe Tyr Gly Cys
            340   345   350

Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp Cys Val Asp Lys
            355   360   365

Met Leu Ile Trp Trp Glu Glu Gly Lys Met Thr Asn Lys Val Val Glu
  370   375   380

Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg Val Asp Gln Lys
385   390   395   400

Cys Lys Ser Ser Val Gln Ile Asp Ser Thr Pro Val Ile Val Thr Ser
            405   410   415

Asn Thr Asn Met Cys Val Val Val Asp Gly Asn Ser Thr Thr Phe Glu
            420   425   430

His Gln Gln Pro Leu Glu Asp Arg Met Phe Lys Phe Glu Leu Thr Lys
            435   440   445

Arg Leu Pro Pro Asp Phe Gly Lys Ile Thr Lys Gln Glu Val Lys Asp
  450   455   460

Phe Phe Ala Trp Ala Lys Val Asn Gln Val Pro Val Thr His Glu Phe
465   470   475   480

Lys Val Pro Arg Glu Leu Ala Gly Thr Lys Gly Ala Glu Lys Ser Leu
            485   490   495

Lys Arg Pro Leu Gly Asp Val Thr Asn Thr Ser Tyr Lys Ser Leu Glu
            500   505   510

Lys Arg Ala Arg Leu Ser Phe Val Pro Glu Thr Pro Arg Ser Ser Asp
            515   520   525

Val Thr Val Asp Pro Ala Pro Leu Arg Pro Leu Asn Trp Asn Ser Arg
  530   535   540

Leu Val Gly Arg Ser Trp
545   550

<210> 15
<211> 1690
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/Note =
     synthetic construct

<400> 15

```
attctttgct ctggactgct agaggaccct cgctgccatg gctaccttct atgaagtcat    60
tgttcgcgtc ccatttgacg tggaggaaca tctgcctgga atttctgaca gctttgtgga   120
ctgggtaact ggtcaaattt gggagctgcc tccagagtca gatttaaatt tgactctggt   180
tgaacagcct cagttgacgg tggctgatag aattcgccgc gtgttcctgt acgagtggaa   240
caaattttcc aagcaggagt ccaaattctt tgtgcagttt gaaaagggat ctgaatattt   300
tcatctgcac acgcttgtgg agacctccgg catctcttcc atggtcctcg gccgctacgt   360
gagtcagatt cgcgcccagc tggtgaaagt ggtcttccag ggaattgaac cccagatcaa   420
cgactgggtc gccatcacca aggtaaagaa gggcggagcc aataaggtgg tggattctgg   480
gtatattccc gcctacctgc tgccgaaggt ccaaccggag cttcagtggg cgtggacaaa   540
cctggacgag tataaattgg ccgccctgaa tctggaggag cgcaaacggc tcgtcgcgca   600
gtttctggca gaatcctcgc agcgctcgca ggaggcggct tcgcagcgtg agttctcggc   660
tgacccggtc atcaaaagca agacttccca gaaatacatg gcgctcgtca actggctcgt   720
ggagcacggc atcacttccg agaagcagtg gatccaggaa aatcaggaga gctacctctc   780
cttcaactcc accggcaact ctcggagcca gatcaaggcc gcgctcgaca acgcgaccaa   840
aattatgagt ctgacaaaaa gcgcggtgga ctacctcgtg gggagctccg ttcccgagga   900
catttcaaaa aacagaatct ggcaaatttt tgagatgaat ggctacgacc cggcctacgc   960
gggatccatc ctctacggct ggtgtcagcg ctccttcaac aagaggaaca ccgtctggct  1020
ctacggaccc gccacgaccg gcaagaccaa catcgcggag gccatcgccc acactgtgcc  1080
cttttacggc tgcgtgaact ggaccaatga aaactttccc tttaatgact gtgtggacaa  1140
aatgctcatt tggtgggagg agggaaagat gaccaacaag gtggttgaat ccgccaaggc  1200
catcctgggg ggctcaaagg tgcgggtcga tcagaaatgt aaatcctctg ttcaaattga  1260
ttctacccct gtcattgtaa cttccaatac aaacatgtgt gtggtggtgg atgggaattc  1320
cacgaccttt gaacaccagc agccgctgga ggaccgcatg ttcaaatttg aactgactaa  1380
gcggctcccg ccagattttg gcaagattac taagcaggaa gtcaaggact tttttgcttg  1440
ggcaaaggtc aatcaggtgc cggtgactca cgagtttaaa gttcccaggg aattggcggg  1500
aactaaaggg gcggagaaat ctctaaaacg cccactgggt gacgtcacca atactagcta  1560
taaaagtctg gagaagcggg ccaggctctc atttgttccc gagacgcctc gcagttcaga  1620
cgtgactgtt gatcccgctc ctctgcgacc gctcaattgg aattcaagat tggttggaag  1680
aagttggtga                                                         1690
```

<210> 16
<211> 145
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
     synthetic construct

<400> 16

```
ccatcaccaa ggtaaagaag ggcggagcca ataaggtggt ggattctggg tatattcccg    60
cctacctgct gccgaaggtc caaccggagc ttcagtgggc gtggacaaac ctggacgagt   120
ataaattggc cgccctgaat ctgga                                         145
```

<210> 17
<211> 174
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
     synthetic construct

<400> 17

```
taagcaggaa gtcaaggact tttttgcttg ggcaaaggtc aatcaggtgc cggtgactca      60
cgagtttaaa gttcccaggg aattggcggg aactaaaggg gcggagaaat ctctaaaacg     120
cccactgggt gacgtcacca atactagcta taaaagtctg gagaagcggg ccag           174
```

<210> 18
<211> 187
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
      synthetic construct

<400> 18
```
cactctcaag caaggggggtt ttgtaagcag tgatgtcata atgatgtaat gcttattgtc      60
acgcgatagt taatgattaa cagtcatgtg atgtgtttta tccaatagga agaaagcgcg     120
cgtatgagtt ctcgcgagac ttccggggta taaaagaccg agtgaacgag cccgccgcca     180
ttctttg                                                              187
```

<210> 19
<211> 168
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
      synthetic construct

<400> 19
```
aaacctcctt gcttgagagt gtggcactct cccccctgtc gcgttcgctc gctcgctggc      60
tcgtttgggg gggtggcagc tcaaagagct gccagacgac ggccctctgg ccgtcgcccc     120
cccaaacgag ccagcgagcg agcgaacgcg acaggggga gagtgcca                  168
```

<210> 20
<211> 168
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
      synthetic construct

<400> 20
```
aaacctcctt gcttgagagt gtggcactct cccccctgtc gcgttcgctc gctcgctggc      60
tcgtttgggg gggcgacggc cagagggccg tcgtctgccg gctctttgag ctgccacccc     120
cccaaacgag ccagcgagcg agcgaacgcg acaggggga gagtgcca                  168
```

<210> 21
<211> 8
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
      synthetic construct

<400> 21
```
cggtgtga
```

<210> 22
<211> 8
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
       synthetic construct

<400> 22   8
cggttgag

<210> 23
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
       synthetic construct

<400> 23   21
caaaacctcc ttgcttgaga g